

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 15:09:02 ; Search time 22 Seconds
(without alignments)
152.708 Million cell updates/sec

Title: US-09-924-102-2

Sequence: 1 MLSTHFLFTFLFTFLSYSL.....RWGGGGRGRTADTGGMFLS 81

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	16.3	462	1	SR54_HAEIN
2	68	16.3	511	1	COPD_HUMAN
3	67	16.0	829	1	TOP1_XENLA
4	65	15.6	65	1	RPR_DROME
5	65	15.6	386	1	R887_DROME
6	64.5	15.4	365	1	R851_HUMAN
7	64	15.3	511	1	COPD_BOVIN
8	64	15.3	765	1	TOP1_HUMAN
9	64	15.3	767	1	TOP1_MOUSE
10	63.5	15.2	389	1	DNMT_HAICU
11	63.5	15.2	391	1	DNMT_HAICU
12	62	14.8	1898	1	TRHY_HUMAN
13	61.5	14.7	268	1	EP34_HCMVA
14	61.5	14.7	272	1	RS2_CAEEL
15	61.5	14.7	684	1	EP84_HCMVA
16	61.5	14.7	824	1	ROU_HUMAN
17	61	14.6	78	1	DMG1_PHYBI
18	61	14.6	404	1	LA_BOVIN
19	61	14.6	486	1	DNAB_HELPJ
20	61	14.6	767	1	TOP1_CRIGR
21	61	14.6	876	1	SYA_SALTI
22	61	14.6	876	1	SYA_SALTY
23	59.5	14.2	165	1	LEI3_GOSHI
24	59.5	14.2	433	1	THC1_METTH
25	59.5	14.2	766	1	EYA_DROME
26	59	14.1	307	1	CC36_CAEEL
27	59	14.1	519	1	ELAY_DROVI
28	59	14.1	524	1	T2FA_XENLA
29	59	14.1	739	1	BCSA_PSEFL
30	59	14.1	1029	1	TK95_RHIME
31	58.5	14.0	140	1	YK91_HALNT
32	58.5	14.0	365	1	R851_MOUSE
33	58.5	14.0	1228	1	ECM_HUMAN

ALIGNMENTS

34	58.5	14.0	2254	1	CCAG_RAT	054898 ratu
35	58.5	14.0	2377	1	CCAG_HUMAN	043497 homo
36	58	13.9	43	1	GRW1_LYCES	001157 lyc
37	58	13.9	79	1	YSZ1_CAEEL	017811 caeno
38	58	13.9	123	1	LSM4_CAEEL	019952 caeno
39	58	13.9	307	1	SP33_SCHPO	014311 schiz
40	58	13.9	327	1	FBRL_MOUSE	P35550 mus
41	58	13.9	390	1	LA_DROME	P40796 dros
42	58	13.9	408	1	LA_HUMAN	P05455 homo
43	58	13.9	409	1	R23B_HUMAN	P54727 homo
44	58	13.9	864	1	YCL8_HUMAN	Q9ULX2 homo
45	58	13.9	943	1	YLW5_CAEEL	P34408 caeno

RESULT 1

SR54_HAEIN

ID SR54_HAEIN STANDARD; PRT; 462 AA.

AC P44518;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Signal recognition particle protein (fifty-four homolog).

GN FPF OR H10106.

OS Haemophilus influenzae.

OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;

OC Haemophilus.

OX NCBI_TaxID=727;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-R4 / KM20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,

RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

RA Utermack T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,

RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghegan N.S.M.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

RA Venter J.C.;

RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";

RL Science 269:496-512(1995).

CC -1- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC

CC PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE

CC RIBOSOMES (BY SIMILARITY).

CC -1- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA

CC MOLECULE AND PROTEIN FPF (BY SIMILARITY).

CC -1- DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN

CC BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL

CC SEQUENCE.

CC -1- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.

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CC EMBL: U32696; AAC21784.1; -

CC HSSP: O07347; IAFH.

CC TIGR: H10106; -

CC InterPro: IPR003593; AAA_ATPase.

CC InterPro: IPR000897; SRP54.

CC InterPro: IPR004125; SRP54_SPB.

CC InterPro: IPR004780; SRP_sub.

CC Pfam: PF00448; SRP54; 1.

CC Pfam: PF02881; SRP54_N; 1.

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DR Pfam: PF02978; SRP_SBP; 1.
DR ProDom; PD000819; SRP54; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRfam; TIGR00959; 3a0501s01; 1.
DR PROSITE; PS00300; SRP54; 1.
KM Signal recognition particle; GTP-binding; RNA-binding;
KW Complete proteome.
FT DOMAIN 1 295 G-DOMAIN.
FT DOMAIN 296 453 M-DOMAIN.
FT NP_BIND 107 114 GTP (BY SIMILARITY).
FT NP_BIND 190 194 GTP (BY SIMILARITY).
FT NP_BIND 248 251 GTP (BY SIMILARITY).
SQ SEQUENCE 462 AA; 50843 MW; 16AC32089A15BF7A CRC64;

Query Match 16.3%; Score 68; DB 1; Length 462;
Best Local Similarity 27.9%; Pred. No. 3.7;
Matches 29; Conservative 14; Mismatches 31; Indels 30; Gaps 5;

QY 3 LSTH-----LFTLYFTLYFLSYSLGDR-----RLCKRTKQOQEQILRQ 43
DB 360 LSEHVNQVDDKMFVEMALINSMTLKERANDPIINGRRRIALSGSTQVDVNLKQ 419
QY 44 SEVLEFRSETLRK-----TGKGRMGQGGGGGTADTGG 79
DB 420 FDEMQRMMKKRKGAKRMKRGQGLMGGLGGLG---LGGMF 460

RESULT 2
COPD_HUMAN
ID COPD_HUMAN STANDARD; PRT; 511 AA.
AC P48444;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coatomer delta subunit (Delta-coat protein) (Delta-COP) (Archain).
DE COPD OR ARCNI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95301274; PubMed=7782067;
RA Radice P., Pennotti V., Jones C., Perry H., Pierotti M.A.,
RA Tunnicliffe A.;
RT "The human archain gene, ARCNI, has highly conserved homologs in rice
and Drosophila.";
RL Genomics 26:101-106(1995).
CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
TO DIVISIVE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI
MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
TRANSPORT OF DILYSINE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER
CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION
FACTORS (ARFs), WHICH ARE SMALL GTP-BINDING PROTEINS; THE COMPLEX
ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE
PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY
SIMILARITY).
CC -1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
CC -1- SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
FAMILY. COPD SUBFAMILY.
CC -----
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CC -----
DR EMBL; X81197; CAA57071.1; -.
DR EMBL; X81196; CAA57072.1; ALT_INIT.
DR Genew; HGNC:649; ARCNI.
DR MIM; 600820; -.
DR InterPro; IPR001392; Clathrin.med.
DR Pfam; PF00928; Adap_comp_sub; 1.
KM Transport; Protein transport; Golgi stack; Membrane; Polymorphism.
FT VARIANT 186 186 F->L (IN DBSNP:682327).
FT VARIANT 309 309 F->N (IN DBSNP:1063124).
SQ SEQUENCE 511 AA; 57210 MW; 4ED1F72D12A7E75 CRC64;

Query Match 16.3%; Score 68; DB 1; Length 511;
Best Local Similarity 21.1%; Pred. No. 4.1;
Matches 20; Conservative 24; Mismatches 29; Indels 22; Gaps 2;

QY 3 LSTHLEFLYFLYFLSYSLGDRRL-----CLRTKQOQEQILR 42
DB 102 ISEHCFDLFADEYALGIREVNLAQRTPEMDSHEKYFRAVRETOERAKAEKR 161
QY 43 OSEVLEFRSETLRKGRMGQGGGGGTADTGG 77
DB 162 KAKEL--QOARDAERQGRKAPGFGGSSAVSGG 194

RESULT 3
TOP1_XENLA
ID TOP1_XENLA STANDARD; PRT; 829 AA.
AC P41512;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA topoisomerase I (EC 5.99.1.2).
DE TOP1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96433160; PubMed=8836188;
RA Pandit S.D., Richard R.E., Sternglanz R., Bogenhagen D.F.;
RT "Cloning and characterization of the gene for the somatic form of DNA
topoisomerase I from Xenopus laevis.";
RL Nucleic Acids Res. 24:3593-3600(1996).
CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
DNA, followed by passage and rejoining.
CC -1- SUBUNIT: MONOMER.
CC -1- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
RELAX ONLY NEGATIVE SUPERCOILS.
CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
AT ONE END OF THE ENZYME-SWEPT DNA STRAND.
CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC TYPE I TOPOISOMERASE FAMILY.
CC -----
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DR EMBL: L07777; AAB36608.1; -
DR HSSP: P11387; I435.
DR InterPro: IPR001631; Topoisomerase_I.
DR Pfam: PF01028; Topoisomerase_I.1.
DR Pfam: PF02819; Topoisomerase_I.1.
DR PRINTS: PR00416; EUPRISMASE1.
DR SMART: SM00435; TOPEUC; 1.
DR PROSITE: PS00176; TOPOISOMERASE_I_EUK; 1.
DR Isomerase: Topoisomerase; DNA-binding.
FT ACT SITE 779 779 DNA_CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 829 AA; 98230 MW; 8D1FE4252A910219 CRC64;

Query Match 16.0%; Score 67; DB 1; Length 829;
Best Local Similarity 30.0%; Pred. No. 8.8;
Matches 18; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 18 YSLGDRALCLRTKQOKEQOILROSEVILRSEPLRTKTKGKGRMGQGGGRTADTNGG 77
DB 500 YETARLRKMCVEKINHTYKEDWKSKEKVRORAVALYFDIKIALNAGNEKEGEGTADTVG 559

RESULT 4
RPR_DROME STANDARD; PRT; 65 AA.
AC Q24475; Q9VVP7;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reaper protein.
GN RPR OR CG4319.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R; TISSUE=EYE imaginal disk;
RX MEDLINE=94225205; PubMed=8171319;
RA White K., Grether M.E., Abrams J.M., Young L., Farrell K., Steller H.;
RT "Genetic control of programmed cell death in Drosophila.";
RL Science 264:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Butts J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idbegwan C.,
RA Jaitai M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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RA Relneft K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 267:185-2195(2000).
CC -1- FUNCTION: PLAYS A CENTRAL AND GLOBAL REGULATORY FUNCTION FOR THE
CC INITIATION OF APOPTOSIS. ECTOPIC EXPRESSION IN THE DEVELOPING EYE
CC RESULTS IN A SMALL EYE OWING TO EXCESS CELL DEATH.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION CORRESPONDS TO THE PATTERN OF
CC PROGRAMMED CELL DEATH IN THE EMBRYO.
CC -1- SIMILARITY: LIMITED AT THE N-TERMINAL, TO HID AND GRIM.
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CC -----
DR EMBL: L31631; AAL18983.1; -
DR EMBL: AE003520; AAF49264.1; -
DR DR Flybase: FBgn0011706; rpr.
KW Apoptosis.
SQ SEQUENCE 65 AA; 7682 MW; 57F231379AFEAE3C CRC64;

Query Match 15.6%; Score 65; DB 1; Length 65;
Best Local Similarity 37.7%; Pred. No. 0.96;
Matches 23; Conservative 11; Mismatches 11; Indels 16; Gaps 4;

QY 16 LYSISGDRARLCLRTKQOKEQOILROSEVILR-----SETLR-----TKGKRGR 62
DB 3 VAFIYPPDQATL-LRRA--EQKEQILRLRESQWRRLAVLLETLRQYTSCHPKGRKSGK 59
QY 63 W 63
DB 60 Y 60

RESULT 5
RBR7_DROME STANDARD; PRT; 386 AA.
AC P48810;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heterogeneous nuclear ribonucleoprotein 87F (HRP36.1 protein) (P11
DE protein).
GN HRP87F OR HRP36.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R and Canton-S; TISSUE=Ovary;
RX MEDLINE=91187645; PubMed=18492577;
RA Haynes S.R., Johnson D., Raychaudhuri G., Beyer A.L.;
RT "The Drosophila HRP87F gene encodes a new member of the A and B hnRNP
RT protein group.";
RL Nucleic Acids Res. 19:25-31(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=92112968; PubMed=1730754;
RA Matunis E.L., Matunis M.J., Dreyfuss G.;

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RT "Characterization of the major hnRNP proteins from Drosophila
RT melanogaster";
RT J. Cell Biol. 116:257-269(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Canton-S; TISSUE=Embryo;
RA MEDLINE=92020124; PubMed=1717937;
RA Hovemann B.T., Dessen E., Mechler H., Mack E.;
RT "Drosophila snRNP associated protein p11 which specifically binds to
RT heat shock puff 93D reveals strong homology with hnRNP core protein
RT A1.";
RT Nucleic Acids Res. 19:4909-4914(1991).
CC -1- FUNCTION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES. COULD BE
CC NEEDED TO ORGANIZE A CONCENTRATION GRADIENT OF A DORSALIZING
CC MORPHOGEN (DM) ORIGINATING IN THE GERMINAL VESICLE.
CC -1- SUBCELLULAR LOCATION: NUCLEAR AND/OR CYTOPLASMIC.
CC -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RNM).
CC -----
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CC -----
DR EMBL; X54803; CA38574.1; -;
DR EMBL; X62636; CA44502.1; -;
DR EMBL; X59691; CA42212.1; -;
DR HSSP; P09651; IUP1.
DR FLYBASE; FBgn0004237; Hrb87F.
DR InterPro; IPR005054; RNA_rec_mot.
DR Pfam; PF00076; Rrm; 2.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS50102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; 2.
KW RNA-binding; Nuclear protein; Ribonucleoprotein; Repeat;
KW Alternative splicing
FT DOMAIN 24 101 RNA-BINDING (RRM) 1.
FT DOMAIN 115 192 RNA-BINDING (RRM) 2.
FT VAAPSPIC 315 374 MISSING (IN ISOFORM HRP36.1).
FT CONFLICT 271 271 S -> T (IN REF. 3).
SQ SEQUENCE 386 AA; 39557 MW; 2036C04D1E3AF7 CRC64;
Query Match 15.6%; Score 65; DB 1; Length 386;
Best Local Similarity 50.0%; Pred. No. 6.5;
Matches 13; Conservative 3; Mismatches 8; Indels 2; Gaps 1;
OY 54 RKTGKGRMGGGGGGTADTGGMF 79
DB 231 RQNG--GGNWGAGAGGGGFGNSGNF 254
RESULT 6
RRSL_HUMAN
ID RRSL_HUMAN STANDARD; PRT; 365 AA.
AC Q15050; O9BUX8; (Rel. 36, Created)
DT 15-JUN-1998 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome biogenesis regulatory protein homolog.
DE RRR OR KIAA0112.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=95308325; PubMed=7788527;
RA Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
RA Tabata S., Ishikawa K.-I., Kawarabayashi Y., Kotani H., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. III.

RT The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RT DNA Res. 2:37-43(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Uterus;
RA Strausberg R.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SUBCELLULAR LOCATION:
RA Scherl A., Couté Y., Deon C., Sanchez J.-C., Diaz J.-J.,
RA Hochstrasser D.;
RT "Proteomic analysis of the nucleolus";
RT (in) Palagi P.M., Sanchez J.-C., Stoecklin R. (eds.);
RT Proceedings of the Swiss Proteomic Society; 2001 Congress Functional
RT Proteomics, pp.124-124, Fontis Media, Lausanne (2001).
CC -1- FUNCTION: Involved in ribosome biogenesis (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -1- SIMILARITY: BELONGS TO THE RRS1 FAMILY.
CC -----
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CC -----
DR EMBL; D25218; BAA04948.1; ALT_INT.
DR EMBL; BC001811; AAH01811.1; -;
DR EMBL; BC013043; AAH13043.1; -;
DR SWISS-2DPAGE; Q15050; HUMAN.
KW Ribosome biogenesis; Nuclear protein.
FT DOMAIN 302 365 ARG/GUY/LYS-RICH.
SQ SEQUENCE 365 AA; 41193 MW; 061C3A6174C2ETC2 CRC64;
Query Match 15.4%; Score 64.5; DB 1; Length 365;
Best Local Similarity 37.5%; Pred. No. 6.9;
Matches 18; Conservative 6; Mismatches 17; Indels 7; Gaps 2;
OY 29 RKTGKGRMGGGGGGTADTGGMF 76
DB 286 RAINKQREDD---QEEAAR-----RMSKGKRRGGGPGKRRGG 326
RESULT 7
COPD_BOVIN
ID COPD_BOVIN STANDARD; PRT; 511 AA.
AC P53619;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coatomer delta subunit (Delta-coat protein) (Delta-COP).
DE COPD.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE OF 2-511 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97011152; PubMed=8858162;
RA Faustelich D., Auerbach S., Orci L., Ravazzola M., Wegehingel S.,
RA Lottspeich F., Stenbeck G., Harter C., Wieland F.T., Tschochner H.;
RT "Architecture of coatomer: molecular characterization of delta-COP
RT and protein interactions within the complex.";
RT J. Cell Biol. 135:53-61(1996).
CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
CC TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
CC CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI

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CC MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER
CC TRANSPORT OF DILYSINE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER
CC CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION
CC FACTORS (ARF5), WHICH ARE SMALL GTP-BINDING PROTEINS; THE COMPLEX
CC ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE
CC PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY
CC SIMILARITY).
CC -1 SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA,
CC BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS.
CC -1 SUBCELLULAR LOCATION: THE COATOMER IS CYTOPLASMIC OR POLYMERIZED
CC ON THE CYTOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE
CC VESICLES/BUDS ORIGINATING FROM IT (BY SIMILARITY).
CC -1 TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1 SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY. COPD SUBFAMILY.
CC -----
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CC
CC DR EMBL; X94265; CAA63941.1; -.
CC DR InterPro; IPR001392; Clathrn_med.
CC DR Pfam; PF00928; Adap_comp_sub; 1.
CC DR Transport; Protein transport; Golgi stack; Membrane.
CC KW SEQUENCE 511 AA; 57274 MW; 6A285798F25C0CF CnC64;
CC
CC Query Match 15.3%; Score 64; DB 1; Length 511;
CC Best Local Similarity 20.0%; Pred. No. 11;
CC Matches 19; Conservative 24; Mismatches 30; Indels 22; Gaps 2;
CC
CC QY 3 LSTHLFLYFLFYFYSYSGDARL-----CLRTKQOQKQOOLR 42
CC Db 102 ISEHCFLDIFAFDELVALGIVENYNLAQIRFTEDMSHEEYFAVAVRETQREKAEKRR 161
CC QY 43 QSEVLFKRSSETLRKTKGKGRMGQGGGGRGTADTGG 77
CC Db 162 KAKEL--QQAARDAEROGKKAPEGGRGSSSVSGG 194
CC
CC RESULT 8
CC TOP1_HUMAN STANDARD: PRT; 765 AA.
CC AC P11387; OGUJNO; Q12855; Q12856; O43256;
CC 01-JUL-1989 (Rel. 11, Created)
CC 16-OCT-2001 (Rel. 40, Last sequence update)
CC 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE DNA topoisomerase I (EC 5.99.1.2).
CC GN TOP1.
CC OS Homo sapiens (Human).
CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC CC NCBI_Taxid:9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE-88190108; PubMed-2833744;
CC RA D'Arpa P., Machlin P.S., Rattie H. III, Rothfield N.F.,
CC RA Cleveland D.W., Earnshaw W.C.;
CC RT "cDNA cloning of human DNA topoisomerase I: catalytic activity of a
CC RT 67.7-kDa carboxyl-terminal fragment.";
CC RL Proc. Natl. Acad. Sci. U.S.A. 85:2543-2547(1988).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE-91236733; PubMed-1851751;
CC RA Kunze N., Yang G., Dolberg M., Sundard R., Knippers R., Richter A.;
CC RT "Structure of the human type I DNA topoisomerase gene.";
CC RL J. Biol. Chem. 266:9610-9616(1991).
CC RN [3]
CC RP SEQUENCE OF 5-765 FROM N.A., AND VARIANTS T-370 AND SER-722.
CC KC TISSUE=peripheral blood;

```

RX MEDLINE=95180170; PubMed=7802333,
 RA Fujimori A., Harkey W.G., Kohlhaagen G., Hoki Y., Pommer Y.;
 RT "Mutation at the catalytic site of topoisomerase I in CEM/CC2, a human
 RL leukemia cell line resistant to camptothecin.";
 RN Cancer Res. 55:1339-1346(1995).
 [4]
 RN SEQUENCE OF 1-436 FROM N.A.
 RA Skuce C.;
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 541-765 FROM N.A.
 RA MEDLINE=89288043; PubMed=2544263;
 RA Zhou B.-S., Bastow K.F., Cheng Y.C.;
 RT "Characterization of the 3' region of the human DNA topoisomerase I
 gene.";
 RL Cancer Res. 49:3922-3927(1989).
 [6]
 RN SEQUENCE OF 657-765 FROM N.A.
 RA MEDLINE=90046823; PubMed=2479024;
 RA Maul G.G., Jimenez S.A., Riggs E., Ziemnicka-Kotula D.;
 RT "Determination of an epitope of the diffuse systemic sclerosis marker
 RT antigen DNA topoisomerase I: sequence similarity with retroviral
 RT p30gag protein suggests a possible cause for autoimmunity in systemic
 RL sclerosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8492-8496(1989).
 [7]
 RN VARIANTS CPT-RESISTANT.
 RP MEDLINE=91187651; PubMed=1849260;
 RA Tamura H., Koichi C., Yamada R., Ikeda T., Kohei O., Patterson E.,
 RA Keene J.D., Okada K., Kjeldsen E., Nishikawa K.;
 RT "Molecular cloning of a cDNA of a camptothecin-resistant human DNA
 RT topoisomerase I and identification of mutation sites.";
 RL Nucleic Acids Res. 19:69-75(1991).
 [8]
 RN VARIANT CPT-RESISTANT ALA-729.
 RP MEDLINE=93075133; PubMed=1332703;
 RA Kubota N., Kanazawa F., Nishio K., Takeda Y., Ohmori T., Fujiwara Y.,
 RA Terashima Y., Saijo N.;
 RT "Detection of topoisomerase I gene point mutation in CPT-11 resistant
 RL lung cancer cell line.";
 RL Biochem. Biophys. Res. Commun. 188:571-577(1992).
 [9]
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 215-765.
 RP MEDLINE=98155246; PubMed=9488644;
 RA Redinbo M.R., Stewart L., Kuhn P., Champoux J.J., Hol W.G.J.;
 RT "Crystal structures of human topoisomerase I in covalent and
 RT noncovalent complexes with DNA.";
 RL Science 279:1504-1513(1998).
 [10]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 215-765.
 RP MEDLINE=98155254; PubMed=9488652;
 RA Stewart L., Redinbo M.R., Qiu X., Hol W.G.J., Champoux J.J.;
 RT "A model for the mechanism of human topoisomerase I.";
 RL Science 279:1534-1541(1998).
 [11]
 CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
 CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
 CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
 CC DNA, followed by passage and rejoining.
 CC -1- ENZYME REGULATION: SPECIFICALLY INHIBITED BY CAMPTOTHECIN (CPT), A
 CC PLANT ALKALOID WITH ANTITUMOR ACTIVITY.
 CC -1- SUBUNIT: MONOMER.
 CC -1- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH
 CC NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
 CC RELAX ONLY NEGATIVE SUPERCOILS.
 CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
 CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
 CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
 CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC TYPE I TOPOISOMERASE FAMILY.
 CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J03250: AAA61207.1; -
DR EMBL: M60706: AAA61206.1; JOINED.
DR EMBL: M60688: AAA61206.1; JOINED.
DR EMBL: M60689: AAA61206.1; JOINED.
DR EMBL: M60690: AAA61206.1; JOINED.
DR EMBL: M60691: AAA61206.1; JOINED.
DR EMBL: M60692: AAA61206.1; JOINED.
DR EMBL: M60693: AAA61206.1; JOINED.
DR EMBL: M60694: AAA61206.1; JOINED.
DR EMBL: M60695: AAA61206.1; JOINED.
DR EMBL: M60696: AAA61206.1; JOINED.
DR EMBL: M60697: AAA61206.1; JOINED.
DR EMBL: M60698: AAA61206.1; JOINED.
DR EMBL: M60699: AAA61206.1; JOINED.
DR EMBL: M60700: AAA61206.1; JOINED.
DR EMBL: M60701: AAA61206.1; JOINED.
DR EMBL: M60702: AAA61206.1; JOINED.
DR EMBL: M60703: AAA61206.1; JOINED.
DR EMBL: M60704: AAA61206.1; JOINED.
DR EMBL: M60705: AAA61206.1; JOINED.
DR EMBL: U07804: AAB60379.1; -
DR EMBL: U07806: AAB60380.1; -
DR EMBL: AL035652: CAB43980.1; -
DR EMBL: X16479: CAA34500.1; ALT_INTL.
DR EMBL: M27913: AAA61208.1; -
DR PIR: A30887: ISHUT1.
DR PDB: 1A31: 19-AUG-98.
DR PDB: 1A35: 26-AUG-98.
DR PDB: 1A36: 12-AUG-98.
DR Aarhus/Ghent-2DPAGE: 610; NEPHE.
DR Genew: HGNC:11986; Top1.
DR MIM: 126420.
DR InterPro: IPR001631; Topisomerase-I.
DR Pfam: PF01028; Topoisomerase_I; 1.
DR Pfam: PF02919; Topoisomerase_I_N; 1.
DR PRINTS: PR00416; EUTPISMRASE1.
DR SMART: SM00435; TOPEUC; 1.
DR PROSITE: PS00176; TOPOISOMERASE_I_EUK; 1.
DR KJ: Isomerase; Topoisomerase; DNA-binding; Polymorphism; 3d-structure.
DR FT: 191 197
DR FT: ACT_SITE 723 723 DNA CLEAVAGE (BY SIMILARITY).
DR FT: VARIANT 370 370 M -> T (IN CPT-RESISTANT CELL LINE CEM/C2).
DR FT: VARIANT 533 533 D -> G (IN CPT-RESISTANT CELL).
DR FT: VARIANT 722 722 N -> S (IN CPT-RESISTANT CELL LINE CEM/C2).
DR FT: VARIANT 729 729 T -> A (IN CPT-RESISTANT CELL).
DR FT: VARIANT 729 729 /FTID-VAR_007531.
DR FT: CONFLICT 145 145 A -> V (IN REF. 1).
DR FT: CONFLICT 145 145 A -> V (IN REF. 1).
DR FT: SEQUENCE 765 AA; 90725 MW; 6FBED540BCF7BE28 CRC64;
DR Query Match 15.3%; Score 64; DB 1; Length 765;
DR Best Local Similarity 30.0%; Pred. No. 17;
DR Matches 18; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
DR 444 YSLGDRARLCKRTKQKQEQQLRQSEVLFNSETLRKTKGKRRGGGCGGAGTADTGG 77
DR 18 YSLGDRARLCKRTKQKQEQQLRQSEVLFNSETLRKTKGKRRGGGCGGAGTADTGG 77
DR 18 YSLGDRARLCKRTKQKQEQQLRQSEVLFNSETLRKTKGKRRGGGCGGAGTADTGG 77
DR 01-OCT-1993 (Rel. 27, Created)

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DR 01-OCT-1993 (Rel. 27, last sequence update)
DR 16-OCT-2001 (Rel. 40, last annotation update)
DR DNA topoisomerase I (EC 5.99.1.2).
DR TOPI OR TOP-1.
DR Mus musculus (Mouse).
DR Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DR Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DR NCBI_TaxID=10090;
DR [1]
DR SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
DR MEDLINE=93216125; PubMed=8096488.
DR Kawai O., Yasui Y., Sakai Y., Watanabe T., Ishii K.,
DR Yanagihara S., Andoh T.,
DR Cloning of the mouse cDNA encoding DNA topoisomerase I and
DR chromosomal location of the gene.
DR Gene 125:211-216(1993).
DR [2]
DR RP SEQUENCE FROM N.A.
DR Hui C.F., Lo C.K., Hwang J.,
DR Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
DR -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
DR CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
DR -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
DR DNA, followed by passage and rejoining.
DR -1- SUBUNIT: MONOMER.
DR -1- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND IT CAN RELAX BOTH
DR NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES
DR RELAX ONLY NEGATIVE SUPERCOILS.
DR -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
DR BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
DR WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
DR AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
DR -1- SIMILARITY: BELONGS TO THE EUKARYOTIC TYPE I TOPOISOMERASE FAMILY.
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DR -----
DR EMBL: D10061: BAA00950.1; -
DR EMBL: L20632: AAA40466.1; -
DR PIR: JU0144; JU0144.
DR HSSP: P11387; 1A35.
DR MGD: MGI:98788; Top1.
DR InterPro: IPR001631; Topisomerase-I.
DR Pfam: PF01028; Topoisomerase_I; 1.
DR Pfam: PF02919; Topoisomerase_I_N; 1.
DR PRINTS: PR00416; EUTPISMRASE1.
DR SMART: SM00435; TOPEUC; 1.
DR PROSITE: PS00176; TOPOISOMERASE_I_EUK; 1.
DR KJ: Isomerase; Topoisomerase; DNA-binding.
DR FT: ACT_SITE 725 725 DNA CLEAVAGE (BY SIMILARITY).
DR FT: CONFLICT 91 91 R -> P (IN REF. 2).
DR FT: CONFLICT 121 121 D -> E (IN REF. 2).
DR FT: CONFLICT 129 129 A -> V (IN REF. 2).
DR FT: CONFLICT 161 161 MISSING (IN REF. 2).
DR FT: CONFLICT 167 167 S -> L (IN REF. 2).
DR FT: CONFLICT 277 277 R -> W (IN REF. 2).
DR FT: CONFLICT 292 292 G -> E (IN REF. 2).
DR FT: CONFLICT 522 522 G -> V (IN REF. 2).
DR FT: CONFLICT 533 533 G -> Y (IN REF. 2).
DR FT: CONFLICT 762 762 D -> Y (IN REF. 2).
DR FT: SEQUENCE 767 AA; 90789 MW; 398327062B179F2A CRC64;
DR Query Match 15.3%; Score 64; DB 1; Length 767;
DR Best Local Similarity 30.0%; Pred. No. 17;
DR Matches 18; Conservative 9; Mismatches 33; Indels 0; Gaps 0;
DR 18 YSLGDRARLCKRTKQKQEQQLRQSEVLFNSETLRKTKGKRRGGGCGGAGTADTGG 77
DR 18 YSLGDRARLCKRTKQKQEQQLRQSEVLFNSETLRKTKGKRRGGGCGGAGTADTGG 77
DR 18 YSLGDRARLCKRTKQKQEQQLRQSEVLFNSETLRKTKGKRRGGGCGGAGTADTGG 77
DR 01-OCT-1993 (Rel. 27, Created)

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Db 446 YETARRLKCYDKIRNQRREDWKSXEMKVRQRAVALXIFDKLALRAGNEKEEGEATDTVG 505

RESULT 10

DNAL_HALCU STANDARD; PRT; 389 AA.

AC 034135;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last sequence update)

GN DnaJ OR HSP40.

OS Halobacterium cutirubrum.

OC Archaea: Euryarchaeota: Halobacteriales; Halobacteriales;

OC Halobacteriaceae; Halobacterium.

OX NCBI_TaxID=2242;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33170;

RX MEDLINE=97383250; PubMed=9236279;

RA Bustard K., Gupta R.S.;

RT "The sequences of heat shock protein 40 (DnaJ) homologs provide evidence for a close evolutionary relationship between the

RT Deinococcus-Thermus group and cyanobacteria."

RL J. Mol. Evol. 45:193-205(1997).

CC -1- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH GRPE,

CC THE APPASE ACTIVITY OF DNAK (BY SIMILARITY).

CC -1- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE DNAJ FAMILY.

CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

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CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

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CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

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Best Local Similarity 32.7%; Pred. No. 9.5;
Matches 18; Conservative 5; Mismatches 27; Indels 5; Gaps 1;

RESULT 11

DNAL_HALNI STANDARD; PRT; 391 AA.

AC 034135;

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last sequence update)

GN DnaJ OR VNG0489G.

OS Halobacterium sp. (strain NRC-1).

OC Archaea: Euryarchaeota: Halobacteriales; Halobacteriales;

OC Halobacteriaceae; Halobacterium.

OX NCBI_TaxID=64091;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=20504483; PubMed=11016950;

RA Ng W.V., Kennedy S.P., Mahafas G.G., Bergquist B., Pan M.,

RA Shukla H.D., Laaky S.R., Baliga N.S., Thorsson V., Shroga J.,

RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

RA Leitauer B., Keller K., Cruz R., Danon M.J., Hough D.W.,

RA Madocks D.G., Jablonst P.E., Krebs M.P., Angevine C.M., Dale H.,

RA Isenberger T.A., Peck R.F., Pohlschoder M., Spudich J.L., Jung K.-H.,

RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,

RT "Genome sequence of Halobacterium species NRC-1";

CC -1- FUNCTION: ACTS AS A CO-CHAPERONE. STIMULATES, JOINTLY WITH GRPE,

CC THE APPASE ACTIVITY OF DNAK (BY SIMILARITY).

CC -1- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE DNAJ FAMILY.

CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.

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CC -1- SIMILARITY: CONTAINS 1 CR DOMAIN.


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RESULT 13
EP34_HCMVA STANDARD; PRT; 268 AA.
ID EP34_HCMVA
AC P16768;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Early phosphoprotein P34.
GN U112.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohnl R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson S.C., Ili, Kouzarides T., Martignetti J.A.,
RA Predde E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169."
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX Wang S.K., Duh C.Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND
CC HSV-7 U79 AND HCMV U112 (P34).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X17403; CA35315.1; ALT_TERM.
DR EMBL: U57433; AAB53251.1; -.
DR PIR: S09860; S09860.
DR InterPro: IPR004138; U79_P34.
DR Pfam: PF03064; U79_P34; 1.
KW Early protein; Phosphorylation.
FT DOMAIN 148 153 POLY-GLY.
FT DOMAIN 197 200 POLY-SER.
FT DOMAIN 202 220 POLY-GLY.
SQ SEQUENCE 268 AA; 28142 MW; BD5906FAEAB28FC9 CRC64;

Query Match 14.7%; Score 61.5; DB 1; Length 268;
Best Local Similarity 40.5%; Pred. No. 11;
Matches 17; Conservative 2; Mismatches 20; Indels 3; Gaps 1;

OY 36 KEOQILROSEVLEPSEFLRTKTKGRWGQGGGGRGTADTGG 77
Db 179 EEOQRRROEO---RHEERRKKSSSSAGGGGGGAGGGGGGG 217

RESULT 14
RS2_CAEEL STANDARD; PRT; 272 AA.
ID RS2_CAEEL
AC P51403;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S2.
GN RPS-2 OR C49H3.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.

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RC STRAIN-Bristol N2;
RA Wu X.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U42436; AAF9899.1; -.
DR HSSP: P02357; 1PKP.
DR Wormpep; C49H3.11; CE04237.
DR InterPro: IPR000831; Ribosomal_S5.
DR PIR: P00333; Ribosomal_S5_C.
DR Pfam: PF03719; Ribosomal_S5_C; 1.
DR TIGRFAMs: TIGR01020; rpse_arch; 1.
DR PROSITE: PS00585; RIBOSOML_S5; 1.
KW Ribosomal protein; Repeat.
SQ SEQUENCE 272 AA; 28960 MW; 60049F657DB8CB34 CRC64;

Query Match 14.7%; Score 61.5; DB 1; Length 272;
Best Local Similarity 56.0%; Pred. No. 11;
Matches 14; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

OY 54 RKTGKGRW-GGQGGGRTADTGG 77
Db 27 RPAGRGGRGGRGGRGGRAGRG 51

RESULT 15
EP34_HCMVA STANDARD; PRT; 684 AA.
ID EP34_HCMVA
AC P17151; P87888; O12567;
DT 01-AUG-1990 (Rel. 15, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Early phosphoprotein P84.
GN U112/U113.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90269039; PubMed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohnl R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson S.C., Ili, Kouzarides T., Martignetti J.A.,
RA Predde E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169."
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
RN [2]
RP REVISIONS, AND IDENTIFICATION.
RX Wang S.K., Duh C.Y.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X17403; CA35315.1; -.
DR EMBL: U57432; AAB53251.1; -.
DR PIR: S09860; S09860.
DR InterPro: IPR004138; U79_P34.

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DR Pfam; PF03064; U79_P34; 1.
KW Early protein; Phosphorylation.
FT DOMAIN 148; 153 POLY-GLY.
FT DOMAIN 197 200 POLY-SER.
FT DOMAIN 202 220 POLY-GLY.
FT DOMAIN 271 276 POLY-GLY.
FT DOMAIN 285 296 POLY-GLY.
FT DOMAIN 314 318 POLY-SER.
FT DOMAIN 321 324 POLY-SER.
FT DOMAIN 327 334 POLY-HIS.
FT DOMAIN 390 397 POLY-ALA.
FT DOMAIN 563 568 POLY-SER.
FT DOMAIN 576 576 POLY-SER.
FT DOMAIN 578 585 POLY-PRO.
FT DOMAIN 599 606 POLY-GLY.
FT DOMAIN 615 621 POLY-SER.
SQ SEQUENCE 684 AA; 70272 MW; F3325CE2E29EF449 CRC64;
Query Match 14.78; Score 61.5; DB 1; Length 684;
Best Local Similarity 40.58; Pred. No. 29;
Matches 17; Conservative 2; Mismatches 20; Indels 3; Gaps 1;
OY 36 KEOQILROSEVLFRRSEFLRKTGKRRRWGGGGRGCTADTGG 77
Db 179 EEOQRRRQEQ--RHERRRKSSSSAGGGGGGAGGGGGGG 217

Search completed: May 29, 2003, 15:18:41
Job time : 24 secs